Claims

1. A screening method to determine effective cancer curative medicines, comprising:
   (1) determining position(s) of polymorphic amino acid(s) in amino acids sequence(s), including at least one of DRB1*gene, DQB1*gene, and DPB1*gene of HLA,
   (2) analyzing variations of the polymorphic position(s) of the amino acid(s), and survival results (prognosis, treatment effects) by the cancer treatments [the cancer resection alone (no adjuvant therapy), the anticancer chemotherapy after the cancer resection (Chemotherapy), and the anticancer immunotherapy after the cancer resection (Immunotherapy)],
   (3) determining positions of the amino acids and the amino acid(s), which have been estimated to have a statistically significant relationship with the treatments,
   (4) creating a three-dimensional structure of amino acid sequences including the amino acids, and
   (5) using the interactions of candidate compounds with the three-dimensional structure as a marker.
2. The method according to claim 1, wherein cancer is analyzed by distinguishing stomach cancer and others.
3. The method according to claim 1, which is carried out by utilizing drug designing techniques based on comparison with the three-dimensional structure of the candidate compounds.
4. The method according to claim 1, wherein effective cancer curative medicines can suppress and control metastasis of cancer.
5. The method according to claim 1, wherein effective cancer curative medicines are immunological medicines.
6. The method according to claim 1, wherein effective cancer curative medicines are chemotherapeutic medicines.

7. The method according to claim 1, wherein the effectiveness of the cancer curative medicines is measured by:
   (1) contacting the candidate compounds and the three-dimensional structure by alignment and variation of each amino acid under a condition in which the interaction is possible,
   (2) evaluating the interaction of the three-dimensional structure with the candidate compounds , and detecting a signal of the interaction.
8. The method according to claim 7, wherein cancer is analyzed by distinguishing stomach cancer and other cancers.
9. The method according to claim 1, wherein both effectiveness of the anticancer treatments and the variations of the base sequences coding the polymorphic amino acids on any one of DRB1*gene, DQB1*gene, and DPB1* gene of HLA, are analyzed.
10. The method according to claim 7, wherein both effectiveness of the anticancer treatments and the variations of the base sequences coding the polymorphic amino acids on any one of DRB1*gene, DQB1*gene, and DPB1* gene of HLA, are analyzed.
11. A measuring method for evaluating anticancer treatments, comprising:
   (1) determining position(s) of polymorphic amino acid(s) in amino acids sequence(s), including at least one of DRB1*gene, DQB1*gene, and DPB1*gene of HLA,
   (2) analyzing variations of the polymorphic position(s) of the amino acid(s), and survival results (prognosis, treatment effects) by the cancer treatments [the cancer resection alone (no adjuvant therapy), the anticancer chemotherapy after the cancer resection (Chemotherapy), the anticancer immunotherapy after the cancer resection (Immunotherapy)],
   (3) determining positions of the amino acids and the amino acids, which have been estimated to have a statistically significant relationship with the treatments, and

(4) utilizing the specified positions and the corresponding amino acid(s) as a marker.

12. The method of claim 11, wherein cancer is analyzed by distinguishing stomach cancer from other cancers.

13. A measuring method for evaluating cancer treatments, comprising :

(1) determining position(s) of polymorphic amino acid(s) in amino acids sequence(s), including at least one of, DRB1*gene, DQB1*gene, and DPB1*gene of HLA,

(2) analyzing variations of the base sequences coding the polymorphic positions of the amino acid, and survival results (prognosis, treatment effects) by the cancer treatments [the cancer resection alone (no adjuvant therapy), the anticancer chemotherapy after the cancer resection (Chemotherapy), the anticancer immunotherapy after the cancer resection (Immunotherapy)] ,

(3) determining position(s) of the amino acids and the amino acid(s) which have been estimated to have a statistically significant relationship with the treatments, and the corresponding base sequences, and

(4) utilizing the specified positions and the amino acids together with the corresponding base sequences as a marker.

14. The method according to claim 13 , wherein cancer is analyzed by distinguishing stomach cancer from other cancers.

15. Clinical measuring reagents comprising a composition:

(1) wherein positions of polymorphic amino acid(s) in amino acids sequence(s), that include at least one of, DRB1*gene, DQB1*gene, and DPB1*gene of HLA have been determined,

(2) wherein the variation of the polymorphic positions of the amino acid, and survival results (prognosis, treatment effects) by the cancer treatments [the cancer resection alone (no adjuvant therapy), the anticancer chemotherapy after the cancer resection

(Chemotherapy), the anticancer immunotherapy after the cancer resection (Immunotherapy)] have been analyzed,

(3) wherein the positions of the amino acids and the amino acids, which have been estimated to have a statistically significant relationship with the treatments, have been determined, and

(4) wherein the specified positions and the corresponding amino acids have been used as a marker.

16. The method according to claim 15, wherein cancer is analyzed by distinguishing stomach cancer from other cancers.

17. Clinical measuring reagents comprising a composition:

(1) wherein position(s) of polymorphic amino acid(s) in amino acids sequence(s), that include at least one of DRB1*gene, DQB1*gene, and DPB1*gene of HLA have been determined,

(2) wherein the variations of the base sequences coding the polymorphic positions of the amino acid, and survival results (prognosis, treatment effects) by the cancer treatments [the cancer resection alone (no adjuvant therapy), the anticancer chemotherapy after the cancer resection (Chemotherapy), the anticancer immunotherapy after the cancer resection (Immunotherapy)] have been analyzed,

(3) wherein the positions of the amino acids and the base sequences of amino acids which have been estimated to have a statistically significant relationship with the treatments, and the corresponding base sequences have been determined, and

(4) wherein the specified positions and the amino acids together with the base sequences have been used as a marker.

18. The method according to claim 17, wherein cancer is analyzed by distinguishing stomach cancer from other cancers.